

**STIC Biotechnology Systems Branch**

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/510,698  
Source: PCT/10  
Date Processed by STIC: 7/5/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/570,698

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
    →      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (Sec "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



PCT

## RAW SEQUENCE LISTING

DATE: 07/05/2005

PATENT APPLICATION: US/10/510,698

TIME: 11:16:36

Input Set : A:\MHKBERLIN.ST25.txt

Output Set: N:\CRF4\07052005\J510698.raw

3 <110> APPLICANT: EPIGENOMICS AG  
 4 BERLIN, KURT  
 6 <120> TITLE OF INVENTION: METHOD FOR ANALYSIS OF METHYLATED NUCLEIC ACIDS  
 8 <130> FILE REFERENCE: MHK-051-004  
 10 <140> CURRENT APPLICATION NUMBER: US 10/510,698  
 11 <141> CURRENT FILING DATE: 2004-10-08  
 13 <150> PRIOR APPLICATION NUMBER: PCT/IB03/01791  
 14 <151> PRIOR FILING DATE: 2003-04-09  
 16 <150> PRIOR APPLICATION NUMBER: US 60/370,690  
 17 <151> PRIOR FILING DATE: 2002-04-09  
 19 <160> NUMBER OF SEQ ID NOS: 15  
 21 <170> SOFTWARE: PatentIn version 3.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 22  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Artificial  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: oligonucleotide primer  
 31 <400> SEQUENCE: 1  
 32 ttttcgtcgt tttaggttat cg 22  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 23  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Artificial  
 40 <220> FEATURE:  
 41 <223> OTHER INFORMATION: oligonucleotide primer  
 43 <400> SEQUENCE: 2  
 44 tttttgttgt tttaggttat tgg 23  
 47 <210> SEQ ID NO: 3  
 48 <211> LENGTH: 26  
 49 <212> TYPE: DNA  
 50 <213> ORGANISM: Artificial  
 52 <220> FEATURE:  
 53 <223> OTHER INFORMATION: oligonucleotide probe  
 55 <400> SEQUENCE: 3  
 56 ttccgacgtc gttgttcggt cgatgt 26  
 59 <210> SEQ ID NO: 4  
 60 <211> LENGTH: 23  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Artificial  
 64 <220> FEATURE:  
 65 <223> OTHER INFORMATION: oligonucleotide primer  
 67 <400> SEQUENCE: 4

Does Not Comply  
Affected Diskette Needed

P.3

## RAW SEQUENCE LISTING

DATE: 07/05/2005

PATENT APPLICATION: US/10/510,698

TIME: 11:16:36

Input Set : A:\MHKBERLIN.ST25.txt

Output Set: N:\CRF4\07052005\J510698.raw

```

68 tttttgttgt tttaggttat tgg                23
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 21
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial
76 <220> FEATURE:
77 <223> OTHER INFORMATION: oligonucleotide primer
79 <400> SEQUENCE: 5
80 catatgctgt gaataaatta c                21
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 26
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial
88 <220> FEATURE:
89 <223> OTHER INFORMATION: oligonucleotide probe
91 <400> SEQUENCE: 6
92 tttggatggt gttgtttggt tgatgt          26
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 17
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial
100 <220> FEATURE:
101 <223> OTHER INFORMATION: oligonucleotide primer
103 <400> SEQUENCE: 7
104 cggatacgat ttcgggg                17
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 22
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial
112 <220> FEATURE:
113 <223> OTHER INFORMATION: oligonucleotide primer
115 <400> SEQUENCE: 8
116 atacgataaa cgcaacaacg ac            22
119 <210> SEQ ID NO: 9
120 <211> LENGTH: 29
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial
124 <220> FEATURE:
125 <223> OTHER INFORMATION: oligonucleotide probe
127 <400> SEQUENCE: 9
128 atttggagtt tcgtgattcg cgttacgga      29
131 <210> SEQ ID NO: 10
132 <211> LENGTH: 19
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial
136 <220> FEATURE:
137 <223> OTHER INFORMATION: oligonucleotide primer
139 <400> SEQUENCE: 10
140 tggatatgat tttggggta                19

```

## RAW SEQUENCE LISTING

DATE: 07/05/2005

PATENT APPLICATION: US/10/510,698

TIME: 11:16:36

Input Set : A:\MHKBERLIN.ST25.txt

Output Set: N:\CRF4\07052005\J510698.raw

143 <210> SEQ ID NO: 11  
144 <211> LENGTH: 24  
145 <212> TYPE: DNA  
146 <213> ORGANISM: Artificial  
148 <220> FEATURE:  
149 <223> OTHER INFORMATION: oligonucleotide primer  
151 <400> SEQUENCE: 11  
152 atatgataaa tgcaacaatg acat 24  
155 <210> SEQ ID NO: 12  
156 <211> LENGTH: 29  
157 <212> TYPE: DNA  
158 <213> ORGANISM: Artificial  
160 <220> FEATURE:  
161 <223> OTHER INFORMATION: oligonucleotide probe  
163 <400> SEQUENCE: 12  
164 atttgagatt ttgtgatttg tgttatgga 29  
167 <210> SEQ ID NO: 13  
168 <211> LENGTH: 25  
169 <212> TYPE: DNA  
170 <213> ORGANISM: Artificial  
172 <220> FEATURE:  
173 <223> OTHER INFORMATION: oligonucleotide primer  
175 <400> SEQUENCE: 13  
176 tccatattcc aaaccctata ccaaa 25  
179 <210> SEQ ID NO: 14  
180 <211> LENGTH: 22  
181 <212> TYPE: DNA  
182 <213> ORGANISM: Artificial  
184 <220> FEATURE:  
185 <223> OTHER INFORMATION: oligonucleotide primer  
187 <400> SEQUENCE: 14  
188 tgggattgag ggtaagaggg at 22  
191 <210> SEQ ID NO: 15  
192 <211> LENGTH: 22  
193 <212> TYPE: DNA  
194 <213> ORGANISM: Artificial  
196 <220> FEATURE:  
197 <223> OTHER INFORMATION: (artificial sequence)  
199 <400> SEQUENCE: 15  
200 attagtttcg tttaaggttc ga 22

*insufficient explanation - what is source?*

*(see item 11 on Enr summary sheet)*

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 07/05/2005

PATENT APPLICATION: US/10/510,698

TIME: 11:16:37

Input Set : A:\MHKBERLIN.ST25.txt

Output Set: N:\CRF4\07052005\J510698.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/510,698

DATE: 07/05/2005

TIME: 11:16:37

Input Set : A:\MHKBERLIN.ST25.txt

Output Set: N:\CRF4\07052005\J510698.raw